

FIGURE 1A

1 CCCCCGTCGGTCTTCCACCTCACCTTTTCGAGCTGGCCGCGCTTGCTGTGCGCAGTTTC 60  
61 GGGGACTGGACCTTCCCTGGCTTTTAGCAGCGCCGAGCGCCATGGCGACCCTTTGCTGG 120  
121 GCAGGTGACCGATTCCGGGTGCCCCAAGGAGCTGGCGTGGGTCTGCCCTGCAGCCGCCCCG 180  
181 CCTGGACAGGATGTTTGCTAGAGGGCTGAAGAGGAAATATGGTGACCAGGAAGAAGGAGT 240  
1 M F A R G L K R K Y G D Q E E G V 17  
241 AGAGGGTTTTGGCACTGTCCCTTCCCTATAGCCTGCAGCGACAGTCACTCCTGGACATGTC 300  
E G F G T V P S Y S L Q R Q S L L D M S 37  
301 CCTTGTC AAGCTCCAGCTCTGTACATGCTAGTGAGCCCAATCTCTGCCGCTCGGTCT 360  
L V K L Q L C H M L V E P N L C R S V L 57  
361 CATCGCCAACACAGTCCGGCAGATCCAGGAGGAAATGAGCCAGGATGGTGTGTGGCATGG 420  
I A N T V R Q I Q E E M S Q D G V W H G 77  
421 GATGGCACCCAGAAATGTAGATCGGGCACCAGTTGAACGCCTGGTGTCCACAGAGATCCT 480  
M A P Q N V D R A P V E R L V S T E I L 97  
481 GTGTCGTACAGTGAGGGGAGCTGAGGAAGAGCACCTGCTCCTGAACTGGAAGATGCTCC 540  
C R T V R G A E E E H P A P E L E D A P 117  
541 CTTGCAAAACTCGGTTTCCGAGCTCCCCATCGTTGGCTCAGCACCAGGGCAAAGGAACCC 600  
L Q N S V S E L P I V G S A P G Q R N P 137  
601 TCAGAGCAGCCTCTGGGAGATGGACAGCCCAAGAAAACAGGGGAAGCTTTCAGAAGTC 660  
Q S S L W E M D S P Q E N R G S F Q K S 157  
661 ACTGGACCAGATATTTGAGACCCTGGAGAACAAAACCTCCAGTTCACTGGAGGAACCTCTT 720  
L D Q I F E T L E N K N S S S V E E L F 177  
721 CTCAGATGTGGACAGCTCCTACTATGACCTGGACACAGTGCTAACAGGAATGATGAGTGG 780  
S D V D S S Y Y D L D T V L T G M M S G 197  
781 GACCAAGTCCAGTCTCTGCAATGGCCTTGAGGGCTTTGCTGCAGCCACCCCTCCTCCAG 840  
T K S S L C N G L E G F A A A T P P P S 217  
841 TTCCACTTGCAAGTCTGACCTGGCTGAGCTGGACCATGTGGTAGAGATTCTGGTGGAGAC 900  
S T C K S D L A E L D H V V E I L V E T 237  
901 CTGAGAGGCCACCCAGTGGGCTAAGGGTGAGGCCACCACTCCCCATGGAGCTCACGTGT 960  
\*  
961 GTTGTGACCCAGAGACAGATAAGCACTTGTCCTAAGAGGGGCTCTGGCTCTTGAGCTCAT 1020  
1021 TATCCTTTTGTGTGACATTGGACTCACTGTGGAGGATGGTGTGTACAGCTATGTCTAGT 1080  
1081 CTATTTTCAATTAGATAGGTGAACCTTCTAAAATTAAGTTTTATATGTTTTTGGGCAATA 1140  
1141 TTTTGTCTTAAGATATATTTTTTAACTTTTTTATACCTTTAGATTTTTTTCAGCTATTTTC 1200  
1201 TTAAAAGTATATTTTTTCTACAAACATCCTCTGCTGTACATTAGAAACATTTATAACCT 1260  
1261 AAATACGATTGGTGTGTCTATTTTAAAGTTTAAATAGAAAACCTCTTTTGTACTGAGTC 1320  
1321 TCTACACTCCCAAGGCAACTGTAAATGTAGCCGGCCGGGTGTTTACATGAGAGGCTCCAG 1380  
1381 TATGGTCTACATTCTAGTAGAGCTTGAAAAGAACCATGCACAGCTCCACTGCCCCCTCAC 1440  
1441 TGGGTCTGCTCTGGCGGATCGGAGCTCTTCCCTAGCCCCGTGTGCAGGATGGCTTTATT 1500  
1501 TATGCCTATTTATATGTAAATGCCACTGAAAGCTAAGGTCTTACTCCTGGAAATCCCAAC 1560  
1561 ACCAGTTCTTCAGGGACTGCTGTGAGGCAGTGCCTTATGCAGGTCTTGTCTTGGCCATC 1620  
1621 ACTGTCTGGTTCAGGCCAGCACATGTGACATGAGGACATGACATGCCCCAACCACCCA 1680  
1681 GCACCACATGCTCCATGTCAAGTGTGTACGTGGAGACCCTGGCTCCCAGGCCTGTGCTC 1740  
1741 AGAGAGGGTGTGCAGTCTACGTGTGTGCTGGGGGGGACGACGGTGACCTGTGCTTGCTTGC 1800  
1801 TTTTAAAATGGTGTCTGGACGTTTAAAGTTTAAAACAATCCGACTCCATATGATTTAGG 1860  
1861 GTCCTCCACCCTGGGGTGGCCCCCTATGCTGTCTGCTTGGATCTCAAAGTCTTGGTACTC 1920  
1921 GGCAGTGTGAGACTCCACCCCATGTATCCTTTTTGTCTCTTGTGCTTTTTTGGACTT 1980  
1981 CCCAACCTGAGCCTAAGTTTTATTTTATATGTGCTTCAATATCAACAATGTAAACCTCA 2040  
2041 CTTTATTAAAGTATCCAGCAAATGGAAAAAAAAAAAAAAAAA

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FIGURE 1B

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1  GGGAAAGCTGGCGGCACAGCCGTGGCGCCTGGCTGAGCAGAGGACCCGGCGGGCGGCCTCG      60
61  CGGGTCAGGACACAATGTTTGCACGAGGACTGAAGAGGAAATGTGTTGGCCACGAGGAAG      120
1  M F A R G L K R K C V G H E E D      16
121  ACGTGGAGGGAGCCCTGGCCGGCTTGAAGACAGTGTCTCATACAGCCTGCAGCGGCAGT      180
    V E G A L A G L K T V S S Y S L Q R Q S      36
181  CGCTCCTGGACATGTCTCTGGTGAAGTTGCAGCTTTGCCACATGCTTGTGGAGCCCCAACC      240
    L L D M S L V K L Q L C H M L V E P N L      56
241  TGTGCCGCTCAGTCCTCATTGCCAACACGGTCCGGCAGATCCAAGAGGAGATGACGCAGG      300
    C R S V L I A N T V R Q I Q E E M T Q D      76
301  ATGGACGTGGCGCAGTGGCACCCCTAGGCTGCAGAGCGGGCGCCGCTCGACCGCTTGG      360
    G T W R T V A P Q A A E R A P L D R L V      96
361  TCTCCACGGAGATCCTGTGCCGTGCAGCGTGGGGGCAAGAGGGGGCACATCCTGCTCCTG      420
    S T E I L C R A A W G Q E G A H P A P G      116
421  GCTTGGGGGACGGCCACACACAGGGTCCAGTTTCTGACCTTTGCCCAGTCACCTCAGCAC      480
    L G D G H T Q G P V S D L C P V T S A Q      136
481  AGGCACCAAGGCACCTGCAGAGCAGCGCCTGGGAGATGGATGGCCCTCGAGAAAACAGAG      540
    A P R H L Q S S A W E M D G P R E N R G      156
541  GAAGCTTTCACAAGTCACTTGATCAGATATTTGAAACGCTGGAGACTAAAAACCCAGCT      600
    S F H K S L D Q I F E T L E T K N P S C      176
601  GCATGGAAGAGCTGTTCTCAGACGTGGACAGCCCTACTACGACCTGGACACAGTACTGA      660
    M E E L F S D V D S P Y Y D L D T V L T      196
661  CAGGCATGATGGGGGGTGCCAGGCCGGGCCCTGCGAAGGGCTCGAGGGCTTGGCTCCGG      720
    G M M G G A R P G P C E G L E G L A P A      216
721  CCACCCCAGGCCCTAGCTCCAGCTGCAAGTCCGACCTGGGCGAGCTGGACCACGTGGTGG      780
    T P G P S S S C K S D L G E L D H V V E      236
781  AGATCCTGGTGGAGACCTGAGCAGGAGCCCTGAGTGCTCACAGCCGCTCTGACGCATTG      840
    I L V E T *      241
841  ACACGTGAGCACTGGCTCCCACGGAGGGTGCGCCCTGCCGCCAGCGGCCAGCCTTGCTGC      900
901  CCTGTCTGTGATTCTGAGAAATCCAGAACAGCCATTACCAGTGGGGCTGCAGCCCTA      960
961  GGCCGCTCCCACTCACCTCCCCCTGTGGAGCGCCAGGCAGAGGCTGTTCTGGAAGGCTT      1020
1021  CTTGTCTTCTGACGTCCCCACAGCCCTGGGCCCCCTCGTGTCTCTTTGTGTCCCCACTGT      1080
1081  AGAGGACGGTGAAGCCGAGCTGCATCAACCTCCTTTTACCTTTAGATAGGTGAATTTTAA      1140
1141  CAATTCAGTTTTACATGTTTTTGGGCAGTATTTTGTCTTAAGATATATTTTTTAACTTTT      1200
1201  TATACCTTATCTCTTTAGATTTTTTTCAGCTATTTTCTTAAAAGTATATTTTTTCTATAAA      1260
1261  CATCCTTTGCTGCTACATTAGAACTTTTATAGCCTAAACAATTGCAGTTGGTGTGTTTCA      1320
1321  TTTTTTTAAGGTTTAAATAAGGGTTTTTTGTTTTGTTTTGTTTTTGCAGTGAGCATCAC      1380
1381  TACAGTCTCAGTCAACAGTGTGAATGTATCATGTTTTACTTTAAATGTGTGTGTGATACT      1440
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1501  ACATCTTCCTAGACCTAAGAGTAAATTATGGAGGATTTTATTTATGTCTATTTATATGTA      1560
1561  AATGTCATTGAAGACAAAGGTCAAATATTTGTCTGTTTGTAGATCACAGGCACCAGTTGG      1620
1621  TCTTCAGGGACCTCATAGCCCCCTCGGTGGTGCCTTCTCAAGGCAGTGTTCCTGGAGGCTC      1680
1681  CCATCAGGGTCAGCCCATGCACCTGCCCTGGGTGAGGAAGTAGCATTGCTGCTGGATGAG      1740
1741  AAACGCCCTGCGTGCTCTGTTAGACTGGTGTGAAACAAAAGGTTAAGGCTAGGTTGAAG      1800
1801  TCTAGAATGAAAGAAATCTGAATCCATGTCTATTCATAACCCCTTGATCTGTAGTGTCTATG      1860
1861  GGTGCTGCCGCAGGCAGGGAGTGAGCTGGGGGTGCCTGCAGCCTTCCACTCCTGCCCCGC      1920
1921  CTCACCCACATGCTCCCTGTTTCTCATGCTTTCTCTAACTTCCCTACCCCTTAACCCAA      1980
1981  AAGGTGTGTTTTCTTTTGTGCATATAGCCATTCTTAAATATCAGTGATGTAAACCTCACT      2040
2041  TTATTAATAAAATTATCCAGCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 2

Mouse Hepp	1	MFARGLKRRKYG---DOEEGVGFGTVPSYSLQSQSLDMSLVKLQQLCHMLVEPNLCRSV
Human HEPP	1	MFARGLKRRKCVGHEDVEGALAGLKTVSSYSLQSQSLDMSLVKLQQLCHMLVEPNLCRSV
Mouse Hepp	57	LIANTVRQIQEEMSQDGVVHGMAPONVDRAPVERLVSTEILCRTVRGAEEDHPAPELEDA
Human HEPP	61	LIANTVRQIQEEMTQDGTWRITVAPOAAERAPLDRLVSTEILCRAAWGOEGAHAPAGLGOG
Mouse Hepp	117	PLONSVSELPVGSAPGORNPOSSLWEMDSPQENRGSEFKSLDQIFETLEKNSSVEEL
Human HEPP	121	HTQGPVSDLCPVTSAPRHLQSSAWEMDGPENRGSEFKSLDQIFETLEKNPSCEEL
Mouse Hepp	177	FSDVDSSTYDLDTVLTGMMSCGRSSLCNGLEGFAAATPPSSCKSDLAELDHVVEILVE
Human HEPP	181	FSDVDSPTYDLDTVLTGMMGCARPGPCEGLEGLAPATPGPSSCKSDLAELDHVVEILVE
Mouse Hepp	237	T
Human HEPP	241	T

FIGURE 3

Zebrafish Hepp	1	MFSGTKRKFDGGEETSDGLVAARVASSYSLQSQSLDMSLVKLQQLCHMLVEPNLCRS
Mouse Hepp	1	MFARGLKRRKYG---DOEEGVGFGTVPSYSLQSQSLDMSLVKLQQLCHMLVEPNLCRS
Human HEPP	1	MFARGLKRRKCVGH-EEDVEGALAGLKTVSSYSLQSQSLDMSLVKLQQLCHMLVEPNLCRS
Zebrafish Hepp	61	VLIANTVRQIQEEMTHDGSWHMVTFAFCGASQSPSERLVATEMLCR-----
Mouse Hepp	56	VLIANTVRQIQEEMSQDGVVHGMAPONVDR--APVERLVSTEILCRTVRGAEEDHPAPEL
Human HEPP	60	VLIANTVRQIQEEMTQDGTWRITVAPOAAER--APLDRLVSTEILCRAAWGOEGAHAPAGL

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FIGURE 4A

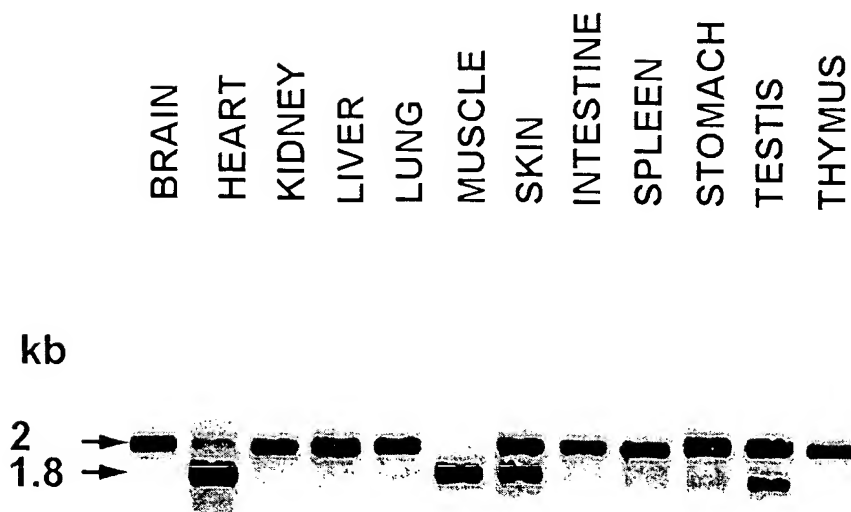
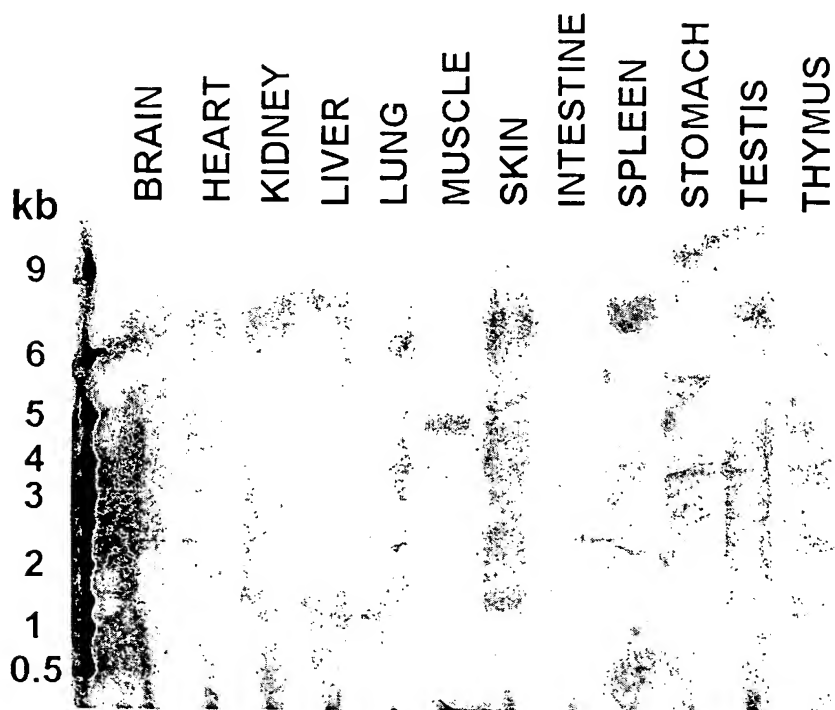


FIGURE 4B



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FIGURE 5

New U.S. Patent Application  
 Inventor: R. JURECIC *et al.*  
 Title: P, A Novel Gene with a Role in  
 Hematopoietic and Neural Development"  
 Attorney Docket No. 39532.176599  
 Sheet 5 of 14

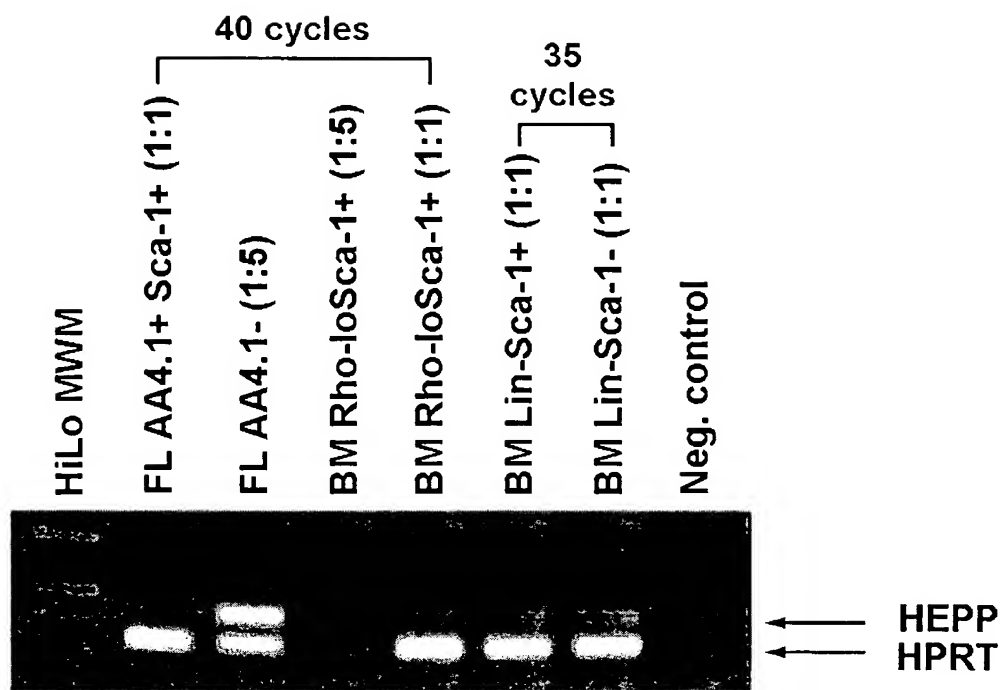


FIGURE 6

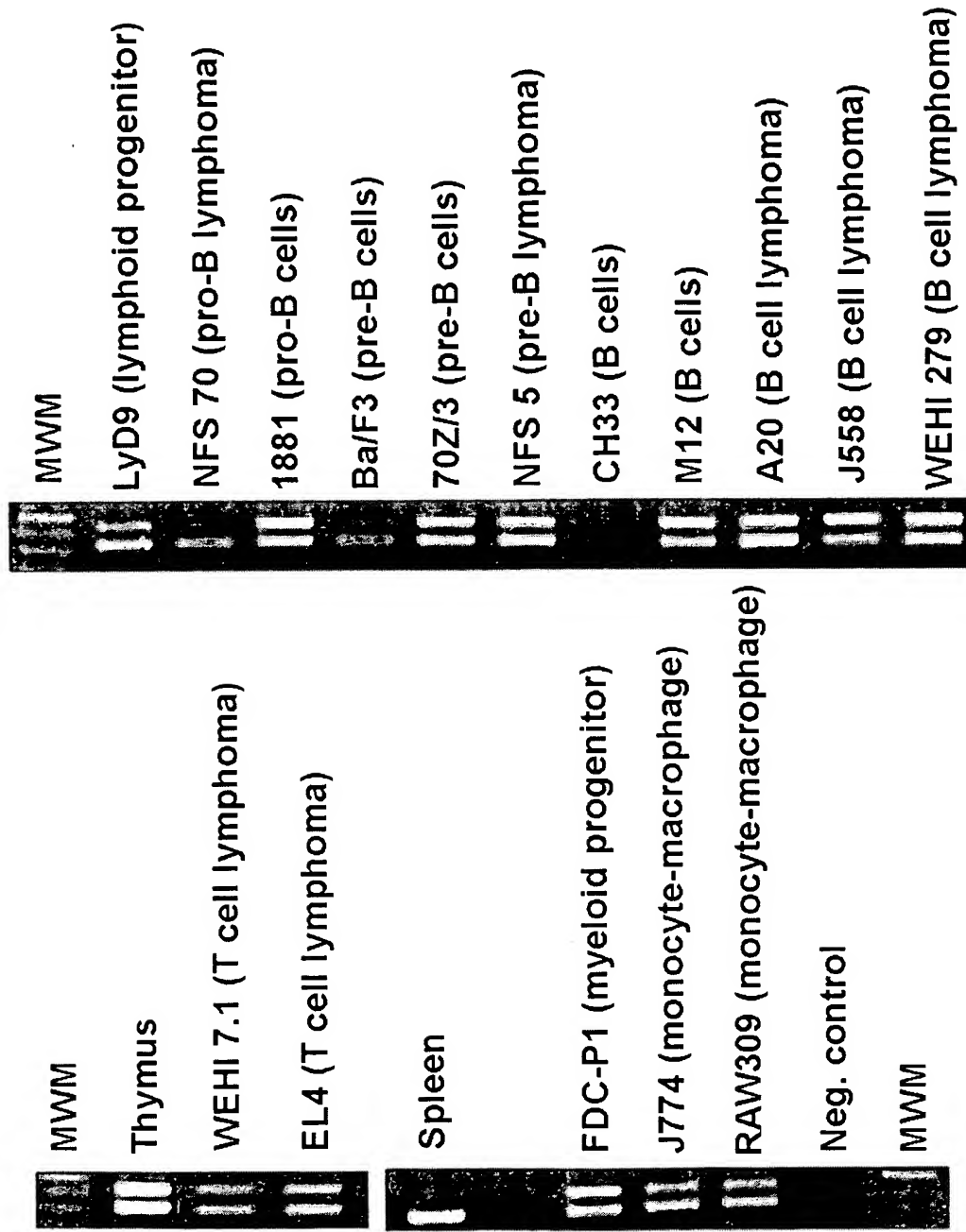
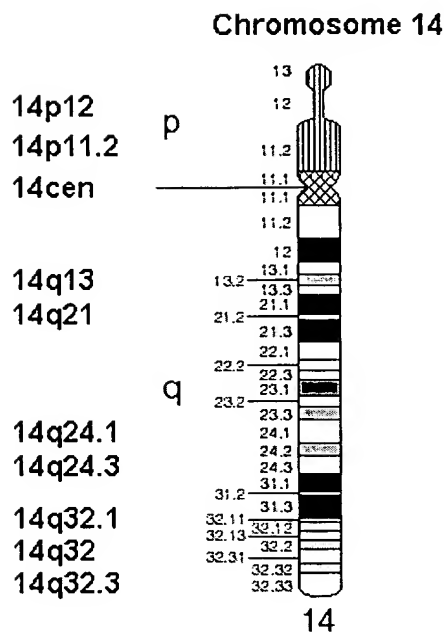


FIGURE 7



translocation breakpoints

FIGURE 8

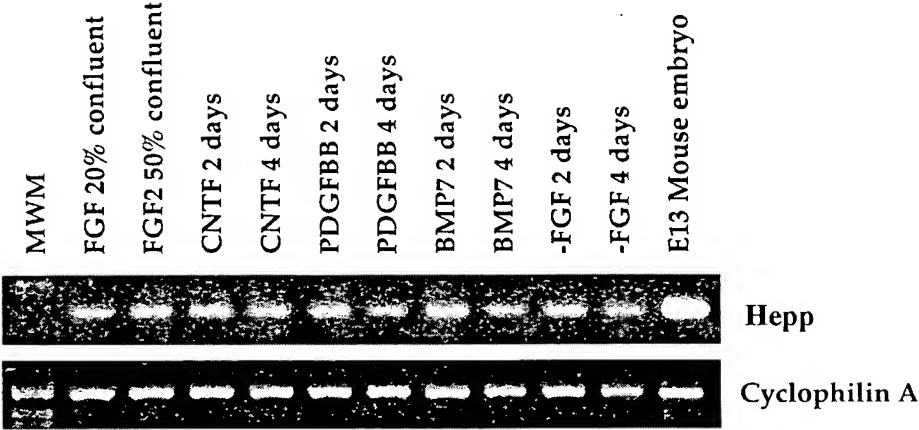
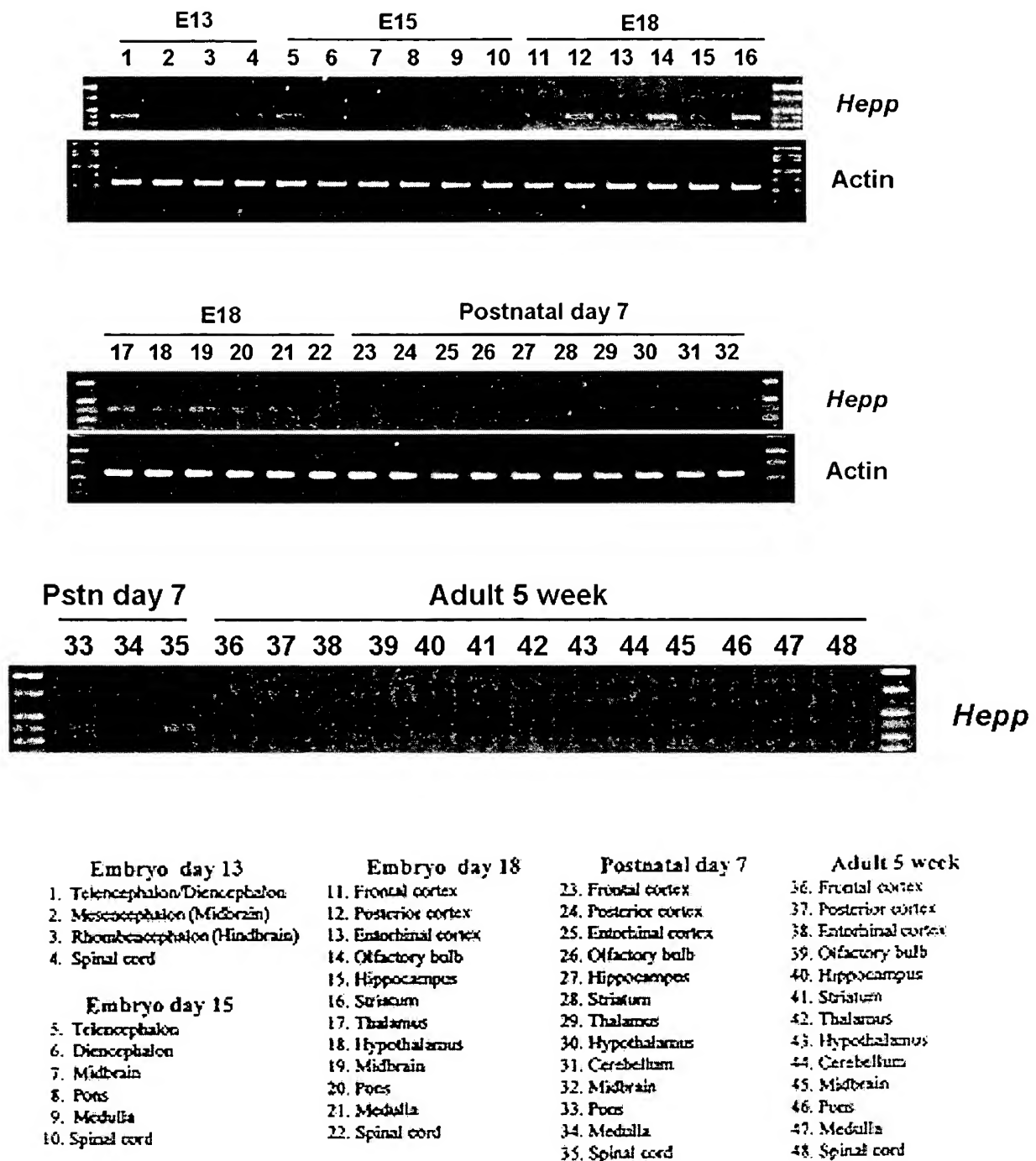




FIGURE 9



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FIGURE 10

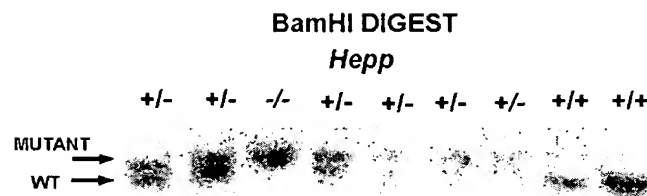
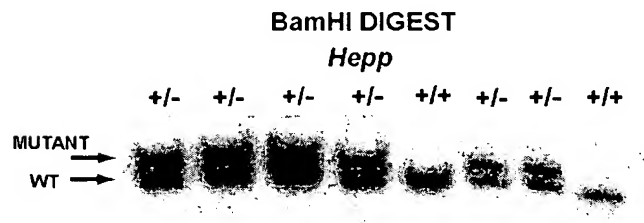


FIGURE 11

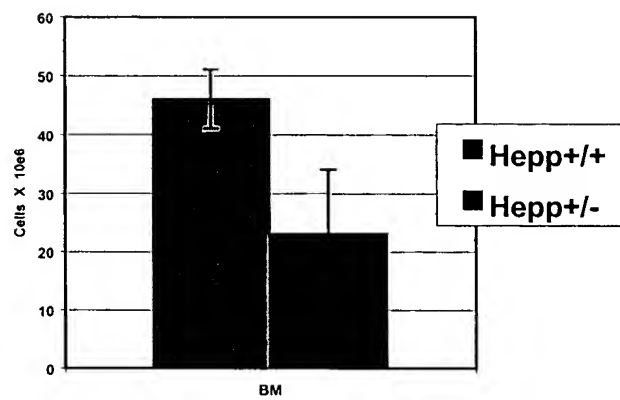


FIGURE 12

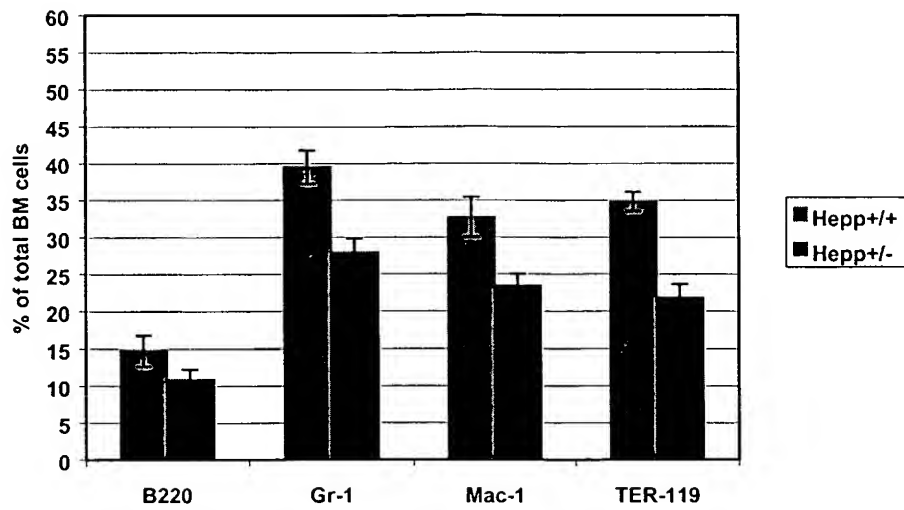


FIGURE 13

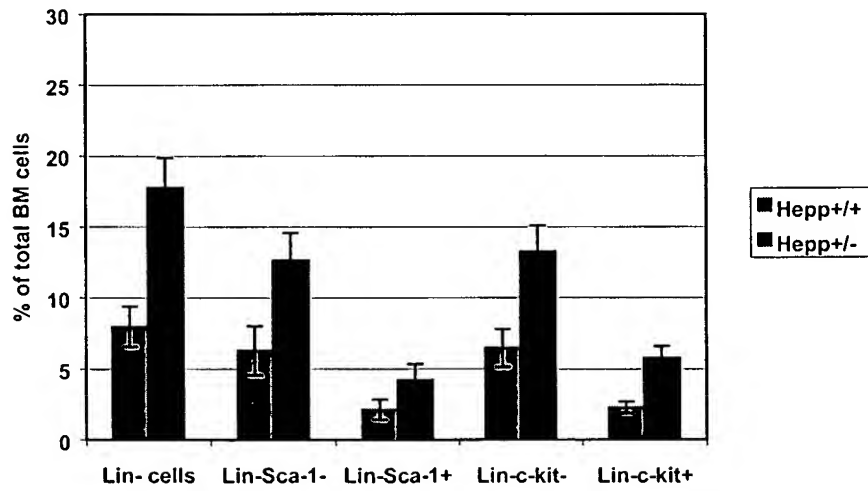


FIGURE 14

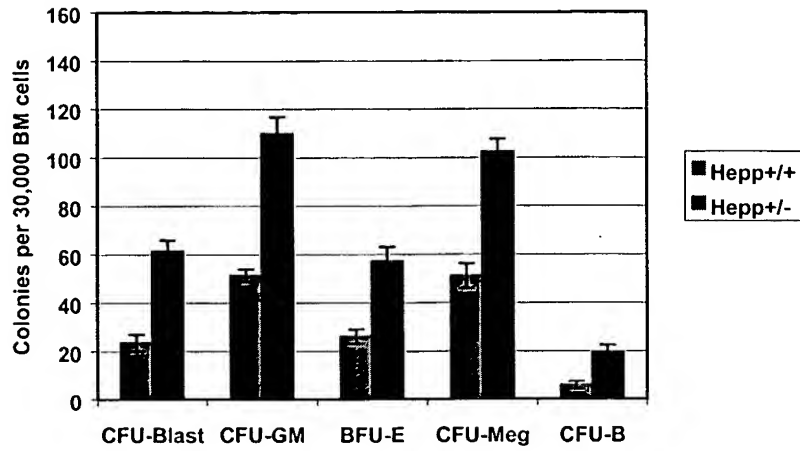


FIGURE 15A-B

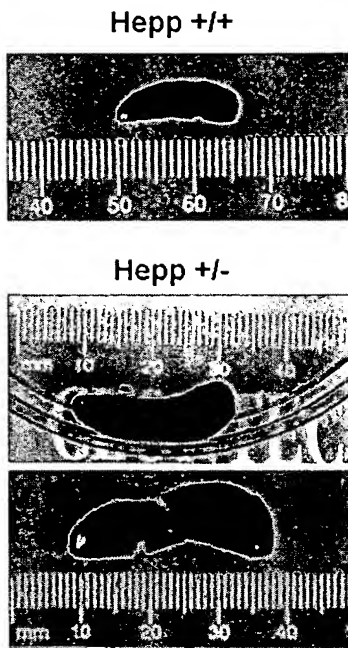


FIGURE 15C

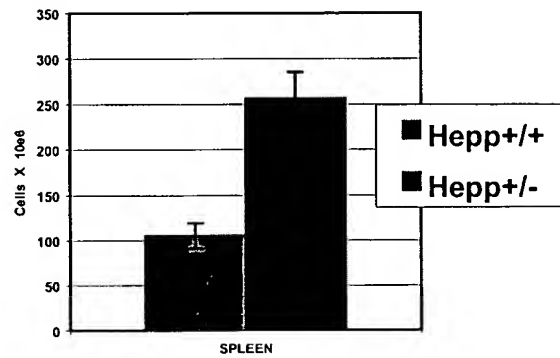


FIGURE 16

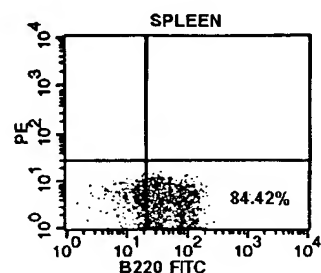
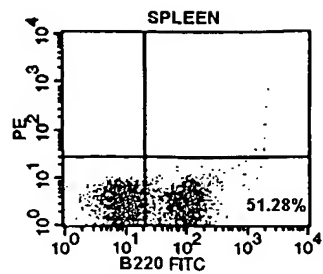
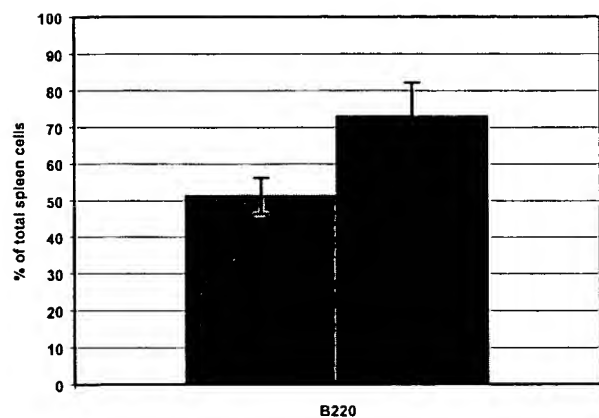


FIGURE 17

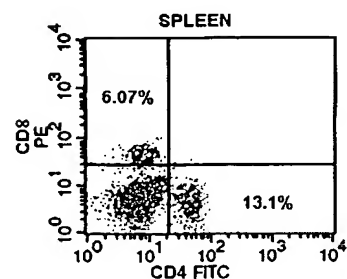
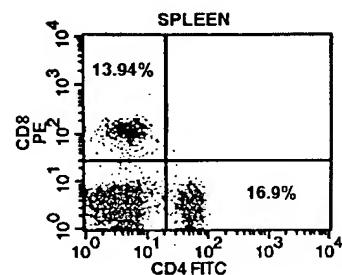
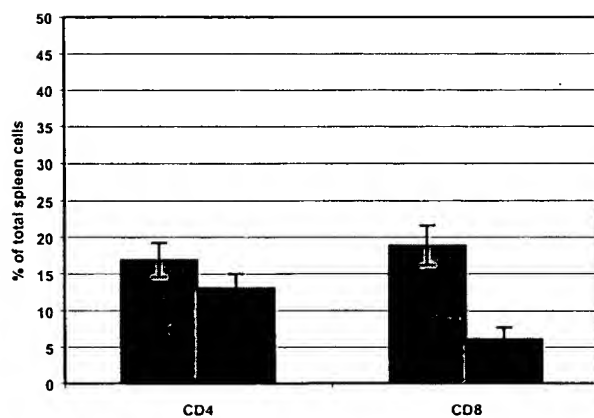


FIGURE 18A



FIGURE 18B



FIGURE 18C



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